

results of BLAST

BLASTN 2.2.9 [May-01-2004]

RID: 1094067506-6429-204335425845.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
2,576,153 sequences; 11,644,915,935 total letters

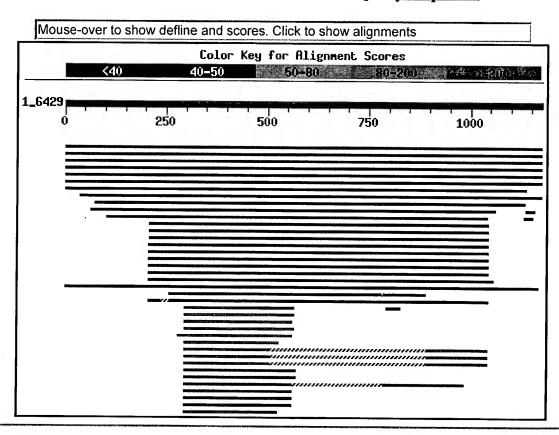
If you have any problems or questions with the results of this search please refer to the ${\bf BLAST}$ ${\bf FAQs}$

Taxonomy_reports

Query=

(1176 letters)

Distribution of 86 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Score E (bits) Value

gi 37181842 gb AY358359.1 Homo sapiens clone DNA66308 ITLN	2261	0.0	LU
<pre>gi 37724011 gb AY157362.1 Homo sapiens intelectin (INTL) m</pre>	2261	0.0	LO
gi 44976128 gb AY549722.1 Homo sapiens omentin mRNA, compl	2250	0.0	
<pre>gi 31542985 ref NM 017625.2 Homo sapiens intelectin 1 (gal</pre>	2238	0.0	L U G
<pre>gi 18088357 gb BC020664.1 Homo sapiens intelectin 1 (galac</pre>	2238	0.0	L U.G
<pre>gi 37724004 gb AY157361.1 Homo sapiens intelectin (INTL) m</pre>	2238	0.0	
<pre>gi 18091782 gb AY065972.1 Homo sapiens endothelial lectin</pre>	2182	0.0	L (U
<u>gi 7019845 dbj AK000029.1 </u> Homo sapiens cDNA FLJ20022 fis,	2179	0.0	LUG
gi 8096220 dbj AB036706.1 Homo sapiens Itln mRNA for intel	2034	0.0	LUG
<pre>gi 20377086 gb AF271386.1 Homo sapiens intestinal lactofer</pre>	<u>1917</u>	0.0	
gi 48146564 emb CR457224.1 Homo sapiens full open reading	1802	0.0	
<u>gi 37182927 gb AY358905.1 </u> Homo sapiens clone DNA108701 ITL	1025	0.0	LU
<pre>gi 37622351 ref NM 080878.2 Homo sapiens intelectin 2 (ITL</pre>	1025	0.0	
<pre>gi 18091784 gb AY065973.1 Homo sapiens endothelial lectin</pre>	1025	0.0	LU
gi 37724015 gb AY157364.1 Mus musculus intelectin (Intl) m	<u>887</u>	0.0	LU
gi 12841003 dbj AK007447.1 Mus musculus 10 day old male pa	887	0.0	LUG
gi 6754387 ref NM 010584.1 Mus musculus intelectin 2 (Itln	<u>858</u>	0.0	LUG
gi 37724013 gb AY157363.1 Mus musculus intelectin (Intl) m	<u>858</u>	0.0	LU
gi 3357908 dbj AB016496.1 Mus musculus mRNA for intelectin	<u>858</u>	0.0	LUG
gi 28932913 gb AY217760.1 Mus musculus intelectin 2 mRNA,	<u>850</u>	0.0	O
gi 22204152 emb AL354714.22 Human DNA sequence from clone gi 18476709 emb AL591806.16 Human DNA sequence from clone	535	e-148	
gi 25046355 gb AC083892.19 Mus musculus chromosome 1 clone	<u>433</u> 329	e-118 9e-87	
gi 49255964 gb BC071079.1 Xenopus laevis cDNA clone MGC:79	169	1e-38	U
gi 2632075 emb X82626.1 XLCORGLEC X.laevis mRNA for cortica	164	5e-37	CONTRACTORS.
gi 20502360 dbj AB061239.1 Xenopus laevis mRNA for lectin	160	8e-36	
gi 1841844 gb U86699.1 XLU86699 Xenopus laevis oocyte lecti	158	3e-35	
gi 49900054 gb BC077059.1 Xenopus tropicalis cDNA clone IM	150	6e-33	O
<u>gi 49115331 gb BC073311.1 </u> Xenopus laevis MGC80711 protein,	135	3e-28	Contract with the
gi 41392401 emb BX571811.5 Zebrafish DNA sequence from clo	133	1e-27	
<pre>qi 38564116 emb BX649532.7 Zebrafish DNA sequence from clo</pre> <pre>gi 49614137 emb BX284688.12 </pre> Zebrafish DNA sequence from cl	$\frac{133}{133}$	1e-27 1e-27	
gi 45360964 ref NM 203519.1 Xenopus tropicalis egg cortica	131	4e-27	LU
gi 25989471 gb AY079196.1 Xenopus tropicalis egg cortical	131	4e-27	
gi 20502358 dbj AB061238.1 Xenopus laevis mRNA for 35 kDa	127	5e-26	CHARLES AND ADDRESS OF THE PARTY OF THE PART
gi 1150691 emb Z50155.1 XLIGF1R X.laevis mRNA for insulin-1	123	7e-25	
gi 38174755 gb BC061445.1 Xenopus tropicalis hypothetical	116	2e-22	Commence.
gi 45360436 ref NM 203598.1 Xenopus tropicalis hypothetica	$\frac{-}{116}$	2e-22	- ALC 20
gi 28971731 dbj AB105372.1 Xenopus laevis XEEL mRNA for em	99	3e-17	
gi 13094238 dbj AB055981.1 Lampetra japonica mRNA for seru	78	6e-11	
<pre>gi 51127570 emb BX511256.9 Zebrafish DNA sequence from clo gi 31790657 dbj AP003327.3 Homo sapiens genomic DNA, chrom</pre>	$\frac{72}{45}$	3e-09	
<u>gi 14916182 gb AC092597.1 </u> Homo sapiens BAC clone RP11-100N	43	0.40 1.5	
gi 16555518 emb AL592144.5 Human DNA sequence from clone R	41	5.8	

Alignments

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Get selected sequences
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                          Deselect all
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\square > qi | 37181842 | qb | AY358359.1 |
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Sbjct: 61
Query: 121
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Query: 181
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Sbjct: 181
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       Sbjct: 241 gaatgtcctagtgcatttgatggcctgtattttctccgcactgagaatggtgttatctac 300
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 $\frac{||\cdot|| ||\cdot|| ||\cdot|| ||\cdot||}{|\cdot||\cdot||} ||\cdot||\cdot||}{|\cdot||\cdot||\cdot||} ||\cdot||\cdot||}$ Homo sapiens intelectin (INTL) mRNA, complete cd Length = 1203

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Strand = Plus / Plus

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Query: Sbjct:	gaggcggccacgagcgatgactacaagaaccctggctactacgacatccaggccaaggac	
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Query: 901
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\square > qi | 44976128 | qb | AY549722.1 |
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Query: 241
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     Length = 1209
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Strand = Plus / Plus
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        Sbjct: 137
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        Sbjct: 437
        aaagcagtctacccagagggggacggcaactgggccaactacaacacctttggatctgca 496
Query: 481
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        Sbjct: 497
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Sbict: 1095 accatgagateccaaggatggagaacaacttacccagtagctagaatgttaatggcagaa 1154

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Sbjct: 557
       ctgaggtaccgcacggacactggcttcctccagacactgggacataatctgtttggcatc 660
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Sbjct: 617
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Query: 661
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Sbjct: 677
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       qccaacqccttqtqtqctqqaatgagggtcaccggatgtaacactgagcatcactgcatt 900
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        Sbjct: 1097 accatgagatcccaaggatggagaacaacttacccagtagctagaatgttaatggcagaa 1156
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        Sbjct: 1157 gagaaaacaataaatcatattgactcaagaaaaaa 1192
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 $[\]square > gi \mid 18091782 \mid gb \mid AY065972.1 \mid$ Length = 1142 Homo sapiens endothelial lectin HL-1 mRNA, compl

Score = 2182 bits (1135), Expect = 0.0
Identities = 1137/1138 (99%)
Strand = Plus / Plus

Query:	1	agaaagctgcactctgttgagctccagggcgcagtggagggag	60
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Query:	61	tgtacccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc	120
Sbjct:	65	tgtacccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc	124
Query:	121	ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaatacttact	180
Sbjct:	125		184
Query:	181	aaggaatggacctgttcttcgtctccatctctgcccagaagctgcaaggaaatcaaagac	240
Sbjct:	185	aaggaatggacctgttcttcgtctccatctctgcccagaagctgcaaggaaatcaaagac	244
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Sbjct:	245		304
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Sbjct:	365		424
Query:	421	aaagcagactacccagaggggacggcaactgggccaactacaacacctttggatctgca	480
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Sbjct:			

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Query: 721
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Sbict: 725
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Sbjct: 845
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Query: 1081 accatgagatcccaaggatggagaacaacttacccagtagctagaatgttaatggcag 1138
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Identities = 1130/1139 (99%)
Strand = Plus / Plus
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Sbjct: 1
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Query: 98
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Sbjct: 61
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Query:	158	cagatgaggctaatacttacttcaaggaatggacctgttcttcgtctccatctctgccca	217
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Strand = Plus / Plus
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        Sbjct: 61
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Query: 375
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